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Fig. 1: DNA and predicted protein sequence of PtCela cDNA

1 GTCGACCCACGCGTCCGTCTTGAAAGGAATATGAAGTTGTAAAGAGCTGGTAAAGTGGTAA 60
61 TAAGCAAGATGATGGAATCTGGGGCTCTATATGCCATACCTGTGGTGAACAGGTGGGGC 120
M M E S G A P I C H T C G E Q V G H
121 ATGATGCAAATGGGGAGCTATTTGTGGCTGCCATGAGTGTAGCTATCCCATGTGCAAGT 180
D A N G E L F V A C H E C S Y P M C K S
181 CTTGTTTCGAGTTTGAAATCAATGAGGGCCGAAAGTTTGTCTGCGGTGTGGCTCGCCAT 240
C F E F E I N E G R K V C L R C G S P Y
241 ATGATGAGAACTTGCTGGATGATGTAGAAAGAAGGGTCTGGCAATCAATCCACAATGG 300
D E N L L D D V E K K G S G N Q S T M A
301 CATCTCACCTCAACGATTCTCAGGATGTCGGAATCCATGCTAGACATATCAGTAGTGTGT 360
S H L N D S Q D V G I H A R H I S S V S
361 CCACTGTGGATAGTGAATGAATGATGAATATGGGAATCCAATTTGGAAGAATCGGGTGA 420
T V D S E M N D E Y G N P I W K N R V K
421 AGAGCTGTAAGGATAAAGAGAACAAGAGAAAAGAGAAGTCTAAGGCTGAAACTGAAC 480
S C K D K E N K K K K R S P K A E T E P
481 CAGCTCAAGTTCCTACAGAACAGCAGATGGAAGAGAAACCGTCTGCAGAGGCTTCGGAGC 540
A Q V P T E Q Q M E E K P S A E A S E P
541 CGCTTTCAATTGTTTATCCAATTCACGCAACAAGCTCACACCATACAGAGCAGTGATCA 600
L S I V Y P I P R N K L T P Y R A V I I
601 TTATGCGACTGGTCATTCTGGGCCTCTTCTTCCACTTCAGAATAACAAATCCTGTGATA 660
M R L V I L G L F F H F R I T N P V D S
661 GTGCCTTTGGCCTGTGGCTTACTTCTGTCAATGTGAGATCTGGTTTGCATTTTCTTGGG 720
A F G L W L T S V I C E I W F A F S W V
721 TGTGATCAGTTCCTCAAGTGAATCCTGTCAATAGAGAAACGTATATCGAAAGGCTGT 780
L D Q F P K W N P V N R E T Y I E R L S
781 CGGCAAGGTATGAAAGAGAGGGTGAGCCTTCTCAGCTTGCTGGTGTGGATTTTTTCGTGA 840
A R Y E R E G E P S Q L A G V D F F V S
841 GTACTGTTGATCCGCTGAAGGAACCGCCATTGATCACTGCCAATACAGTCCTTTCCATCC 900
T V D P L K E P P L I T A N T V L S I L
901 TTGCTGTGGACTATCCCGTCGATAAAGTCTCCTGCTACGTGTCTGATGATGGTGCAGCTA 960
A V D Y P V D K V S C Y V S D D G A A M
961 TGCTTTCATTTGAATCTCTGTAGAAACAGCTGAGTTTGCAAGGAAGTGGGTTCCGTTCT 1020
L S F E S L V E T A E F A R K W V P F C
1021 GCAAAAAATTCTCAATTGAACCAAGAGCACCAGGAGTTTTACTTCTCACAGAAAATTGATT 1080
K K F S I E P R A P E F Y F S Q K I D Y
1081 ACTTGAAAGACAAGGTTCAACCTTCTTTCGTGAAAGAACGTAGAGCAATGAAAAGGGATT 1140
L K D K V Q P S F V K E R R A M K R D Y
1141 ATGAAGAGTACAAAGTCCGAGTTAATGCCCTGGTAGCAAAGGCTCAGAAAACACCTGAAG 1200
E E Y K V R V N A L V A K A Q K T P E E

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1261 GGCATGATTCAGGTCTTCTTGGGAAATACTGGGAGCTCGTGACATTGAAGGAAATGAAC 1320
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1501 TCCTGATGGACCCACAAGTAGGTGAGATGTATGCTATGTGCAGTTCCTCAGAGGTTTG 1560
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1621 TGAAAGGGTTGGATGGCATTCAAGGACCAGTATACGTAGGAAGTGGTTGTGTTTTCAACA 1680
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1681 GGCAAGCACTTTACGGCTACGGGCCTCCTTCTATGCCCAGCTTACGCAAGAGAAAGGATT 1740
Q A L Y G Y G P P S M P S L R K R K D S

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1801 AGGTATACAGAGATGCAAAAAGAGAGGATCTCAATGCTGCCATATTTAATCTTACAGAGA 1860
V Y R D A K R E D L N A A I F N L T E I

1861 TTGATAATTATGACGAGCATGAAAGGTCAATGCTGATCTCCCAGTTGAGCTTTGAGAAAA 1920
D N Y D E H E R S M L I S Q L S F E K T

1921 CTTTGGCTTATCTTCTGTCTTCATTGAGTCTACACTAATGGAGAATGGAGGAGTACCCG 1980
F G L S S V F I E S T L M E N G G V P E

1981 AGTCTGCCAACTCACCACCATTCATCAAGGAAGCGATTCAAGTCATCGGCTGTGGCTATG 2040
S A N S P P F I K E A I Q V I G C G Y E

2041 AAGAGAAGACTGAATGGGAAAAACAGATTGGTTGGATATATGGGTCAGTCACTGAGGATA 2100
E K T E W G K Q I G W I Y G S V T E D I

2101 TCTTAAGTGGCTTCAAGATGCACTGCCGAGGATGGAGATCAATTTACTGCATGCCCGTAA 2160
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2221 GATGGGCTCTTGGTTCTGTGGAAATTTCTTTAGCAGACACTGTCCCCTCTGGTACGGGT 2280
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2281 TTGGAGGAGGCCGTCTTAAATGGCTCCAAAGGCTTGCCTATATAAACACCATTTGTGTACC 2340
G G G R L K W L Q R L A Y I N T I V Y P

2341 CATTTACATCCCTCCCTCTCATTGCCTATTGCACAATTCCTGCAGTTTGTCTGCTCACCG 2400
F T S L P L I A Y C T I P A V C L L T G

2401 GAAAATTCATCATACCAACGCTCTCAAACCTGGCAAGCATGCTGTTTCTTGGCCTCTTTA 2460
K F I I P T L S N L A S M L F L G L F I

2461 TCTCCATCATTGTAAGTGCAGGTGCTTGAAGTAAAGATGGAGCGGTGTCAGCATTGAAGATT 2520

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W R N E Q F W V I G G V S A H L F A V F

2581 TCCAGGGATTCTTAAAAATGTTGGCTGGCATCGATACGAACTTCACTGTCACAGCAAAAG 2640
Q G F L K M L A G I D T N F T V T A K A

2641 CAGCCGAAAGATGCAGAATTTGGGGAGCTATATATGGTCAAGTGGACAACACTTTTGATTC 2700
A E D A E F G E L Y M V K W T T L L I P

2701 CTCCAACCACACTTCTCATTATCAATATGTCGGGTGTGCTGGATTCTCTGATGCACTCA 2760
P T T L L I I N M S G C A G F S D A L N

2761 ACAAAGGATATGAAGCATGGGGCCTCTCTTTGGCAAGGTGTTCTTTGCTTTCTGGGTGA 2820
K G Y E A W G P L F G K V F F A F W V I

2821 TTCTTCATCTCTATCCATTCCCTTAAAGGTCTAATGGGTGCGCCAAAACCTAACACCAACCA 2880
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2881 TTGTTGTTCTCTGGTCAGTGCTGTTGGCCTCTGTCTCTCTCTCGTTTGGGTCAAGATCA 2940
V V L W S V L L A S V F S L V W V K I N

2941 ATCCATTGTTAAACAAAGTTGATAACACCTTGGTTGCGGAGACCTGCATTTCCATTGATT 3000
P F V N K V D N T L V A E T C I S I D C

3001 GCTGAGCTACCTCCAATAAGTCTCTCCCAGTATTTTGGGGTTACAAAACCTTTGGGAATT 3060
*

3061 GGAATATGATCCTCGTTGTAGTTTCCCTCAAGAAAGCACATATCGCTGTCAGTATTTAAA 3120

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3181 AAATACAGGTTTTGATTGTGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3232

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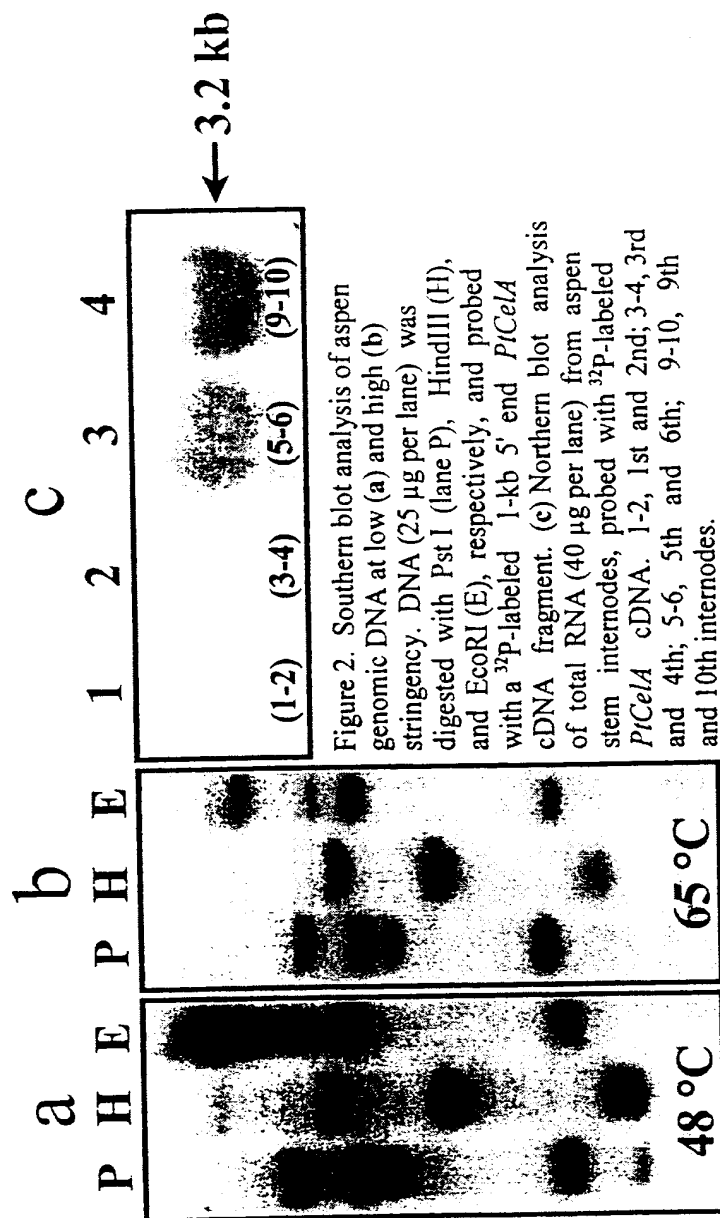


Figure 2. Southern blot analysis of aspen genomic DNA at low (a) and high (b) stringency. DNA (25 µg per lane) was digested with Pst I (lane P), Hind III (H), and EcoRI (E), respectively, and probed with a ³²P-labeled 1-kb 5' end *PtCela* cDNA fragment. (c) Northern blot analysis of total RNA (40 µg per lane) from aspen stem internodes, probed with ³²P-labeled *PtCela* cDNA. 1-2, 1st and 2nd; 3-4, 3rd and 4th; 5-6, 5th and 6th; 9-10, 9th and 10th internodes.

FIG. 2

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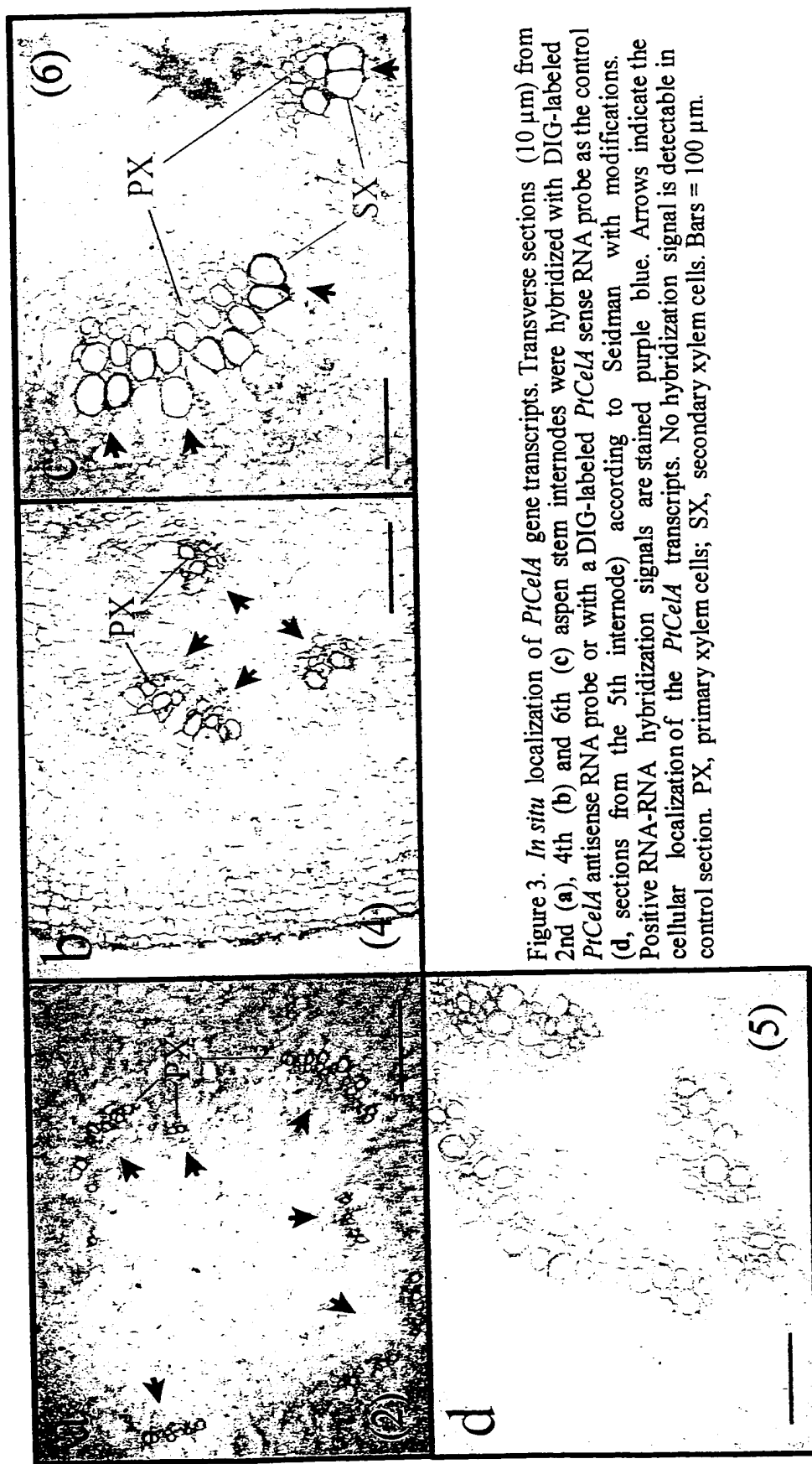


Figure 3. *In situ* localization of *PtCelA* gene transcripts. Transverse sections (10 μ m) from 2nd (a), 4th (b) and 6th (c) aspen stem internodes were hybridized with DIG-labeled *PtCelA* antisense RNA probe or with a DIG-labeled *PtCelA* sense RNA probe as the control (d, sections from the 5th internode) according to Seidman with modifications. Positive RNA-RNA hybridization signals are stained purple blue. Arrows indicate the cellular localization of the *PtCelA* transcripts. No hybridization signal is detectable in control sections. PX, primary xylem cells; SX, secondary xylem cells. Bars = 100 μ m.

FIG. 3

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Fig. 4: DNA sequence of PtCelAP, the 5' flanking region of PtCela coding sequence

```
1  GAATTCGCCCTTTTGAATTCAGGAGACGATAGTTTCCGGTTCGTTGAATGGCTTTGTTCA 60
61  CTTCTGGTCTAGCAATTTGCAAAAGAAGTTACAAAACAAATGCATATTATGTAAATTTAA 120
121 CAAGAGATGGGTTCTATGGTCACTTATTTATGCCCATCATTTGTTCTGGGGTTACTCTTT 180
181 ATAGTCTGATTCGAAGTTGCAAACTGCCGTTTCTGGTATTGCAATTATGTAGCCATAAAC 240
241 TGTTAATCCTGTAGCTATTAGCGGACCAACAACCAGATATACGGGATCAGCGTCGTAAAA 300
301 GAGATCTCCATTCTACGTTTCTTCTAATTTTCCGTTTCAGTGAGAGAATTACCCTGAT 360
361 ACATTGACATGATGATTGATGATTATGGGAACCATCCGATGTTAGACACGAGACCATCT 420
421 GGATCCTGCCAGTTTTCAGTTCACATGGCATCTCAGCCCAAGATCATGTGTTTATACGCC 480
481 TAATGACTTGATTGAAAGTTTGGTAAGTTGAAGATGTGCTCTGCCCAACAGAAACCTTC 540
541 CTTAAATTTCCAGCAAATCTTTCAAACTTGGCCTTACACCCCGAAAATAGACGTGCTTCT 600
601 ACTTGGGTTCTTGGAACCATGCACCAACCGCCATACCCCAACCAACCAACCCCTCAAC 660
661 CTTCTCTTCGCCATTACAAAATGTCAGTACCACCCTCTGAAAGACACCAACACACCCTA 720
721 GCTTTGGTTAGGGTATTTGATATAAAAACAAGGCCAAAACAAAAGATTGGAAGGAAGCAG 780
781 AGGAAGACCCCTCTTGAAAGAATTGAAGTTGTAAAGAGCTGGTAAAGTGGTAATAAGCAAG 840
841 ATGATGGAATCTGGGGCTCCTATATGCCATACCTGTGGTGAACAGGTGGGGCATGATGCA 900
    M M E S G A P I C H T C G E Q V G H D A
901 AATGGGGAGCTATTTGTGGCTTGCCATGAGTGTAGCTATCCCATGTGCAAGTCTTGTTC 960
    N G E L F V A C H E C S Y P M C K S C F
961 GAGTTTGAAATCAAAGAGGGCCGAAAGTTTGCTTGCGGTGTGGCTCGAG 1010
    E F E I K E G R K V C L R C G S
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FIG. 5

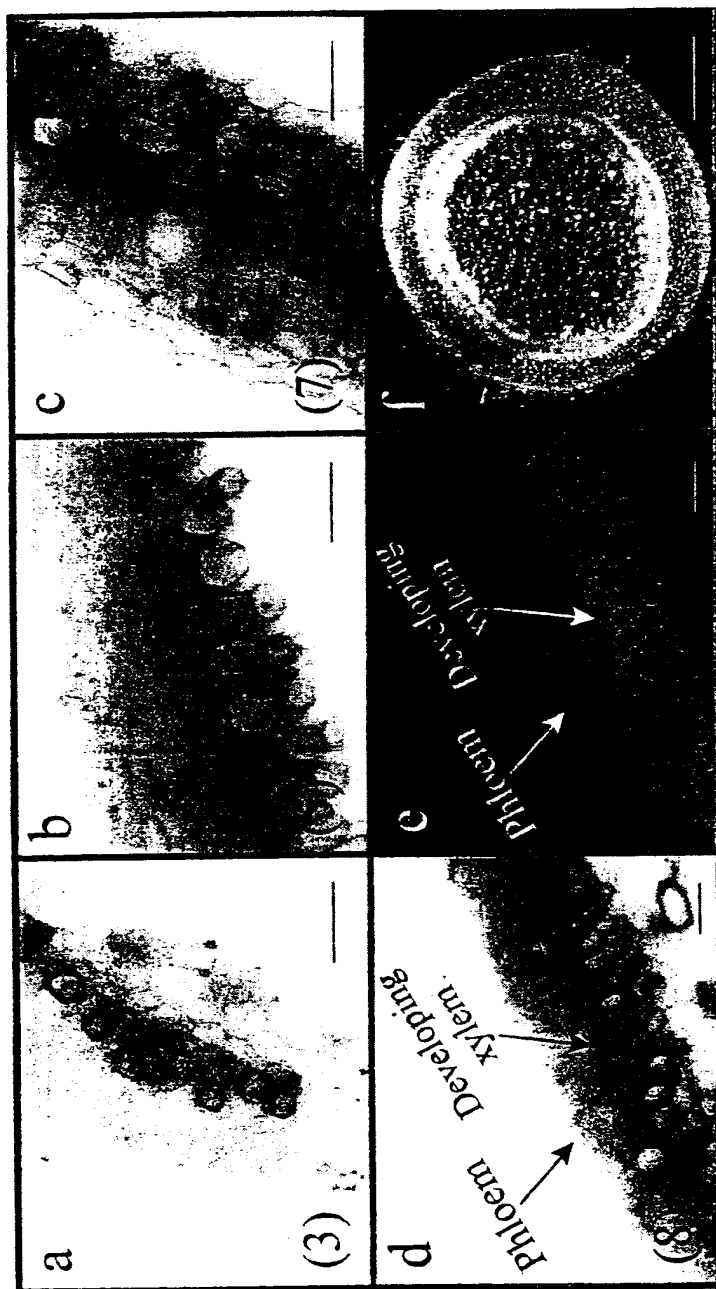


Figure 5. Histochemical analysis of transgenic tobacco for *GUS* gene expression driven by aspen *PtCelA* gene promoter. Stem transverse sections from the 3rd (a), 5th (b), 7th (c), and 8th (d and f) internodes were stained for GUS activity. Fluorescence microscopy (e) showing the identical section as in (d). Lignin autofluorescence was visualized after UV irradiation. An entire section from the 8th internode stained for GUS activity is shown in (f). Bars = 100 μ m in a to e; bar = 1.5 mm in f.

FIG. 6

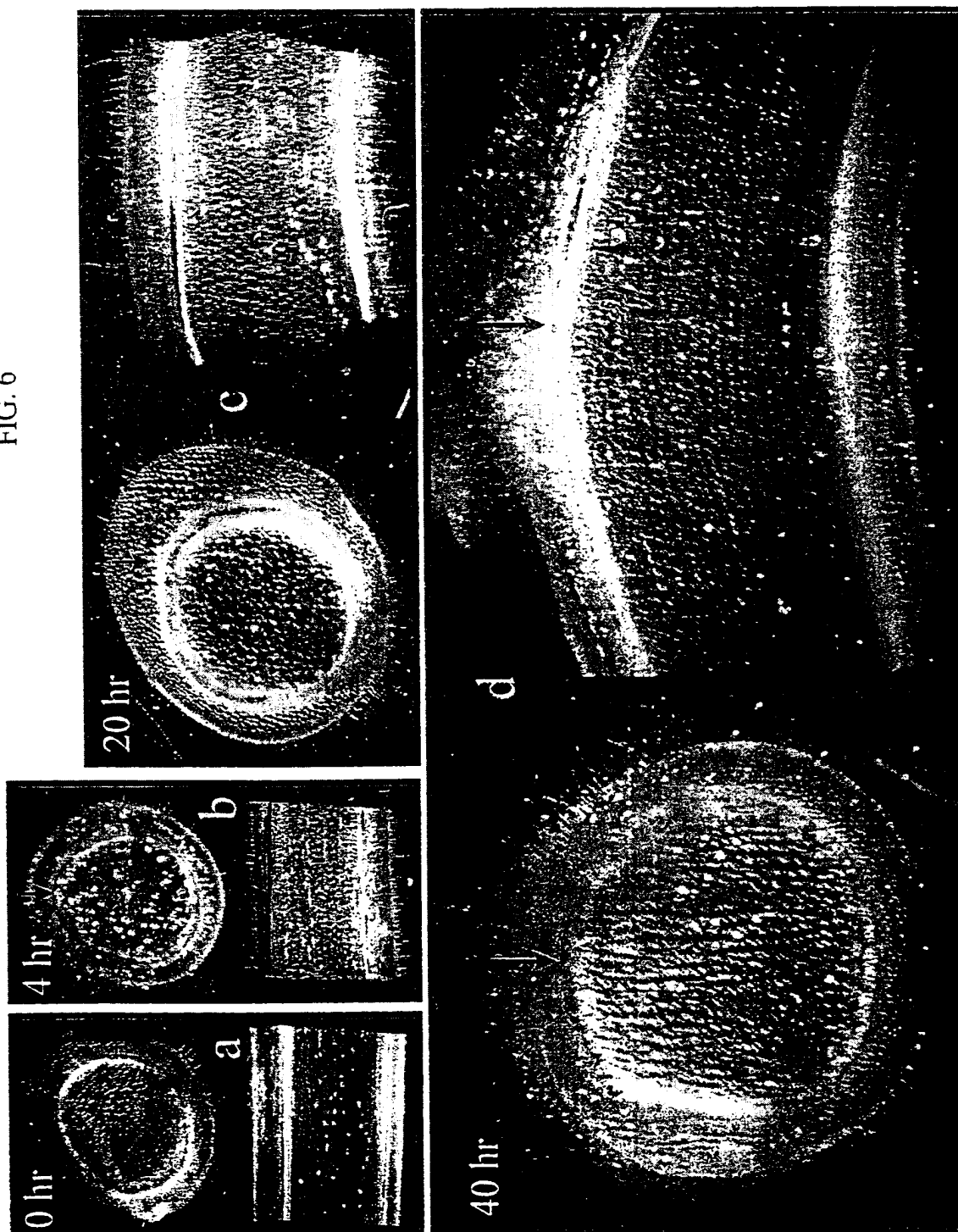


Figure 6. GUS gene expression driven by aspen P_iCelA gene promoter in transgenic tobacco plants under tension stress. Tension stress was induced by bending the transgenic plants. Tangential and longitudinal sections were harvested before bending (a) and 4 (b), 20 (c) and 40 (d) hours after bending and stained for GUS expression. Arrows indicate the bend sites.

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FIG. 7

Arabidopsis thaliana cellulose synthase mRNA SEQ ID NO: 4

```
1 gcgggccgcg ttaatcgccg gttctcacaa caggaatgag tttgtctca ttaatgccga
61 tgagaatgcc cgaataagat cagtcacaaga gctgagtggg cagacatgtc aaatctgcag
121 agatgagatc gaattgactg ttgatggaga accgtttgtg gcatgtaacg aatgtgcatt
181 cccgtgtgtg agaccttgct atgagtacga aagacgagaa ggcaatcaag cttgtccaca
241 gtgcaaaacc cgtttcaaac gtcttaaagg aagtccaaga gttgaagggt atgaagagga
301 agatgacatt gatgatttag acaatgagtt tgagtatgga aataatggga ttggatttga
361 tcagggtttct gaaggatatgt caatctctcg ctacagattcc attgctgact tacggcgacg aggacgttga
421 ggattcagct ccacctggct ctcttattgt tctctcttca cttgggtggc atggcaatag
481 gatttcttct gatagacatg ctcttattgt tctctcttca cttgggtggc atggcaatag
541 agttcatcct gtttctcttt ctgacctgac cgtggctgca catcgaaggc tgatggtacc
601 tcagaaagat cttgcgggtt atggttatgg aagtgtcgct tggaaagatc ggatggagga
661 atggaagaga aagcagaatg agaaacttca gttgtttagg catgaaggag atcctgattt
721 tgaagatggg gatgatgctg attttccaat gatggatgag ggaaggcagc cattgtctat
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841 tgtgattctt ggtctcttct ttcactaccg tattcttcac cccgtcaaa atgcatatgc
901 tttgtggcct atttctgtta tatgtgagat atggtttggc gtttcatggg ttcttgatca
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3301 agagaggtaa gagagatatt gttttacctc taaaagactc cttcattgtg ttcattagat
3361 gatgaaaaa gaaaagaaaa agaagattta atttgttac gagaattgtt atttttgcaa
3421 gaatgtgttg tagatagcgg ccgc
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M 44810F602DXS0131 WPD

FIG. 8

Arabidopsis thaliana cellulose synthase SEQ ID NO: 5

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